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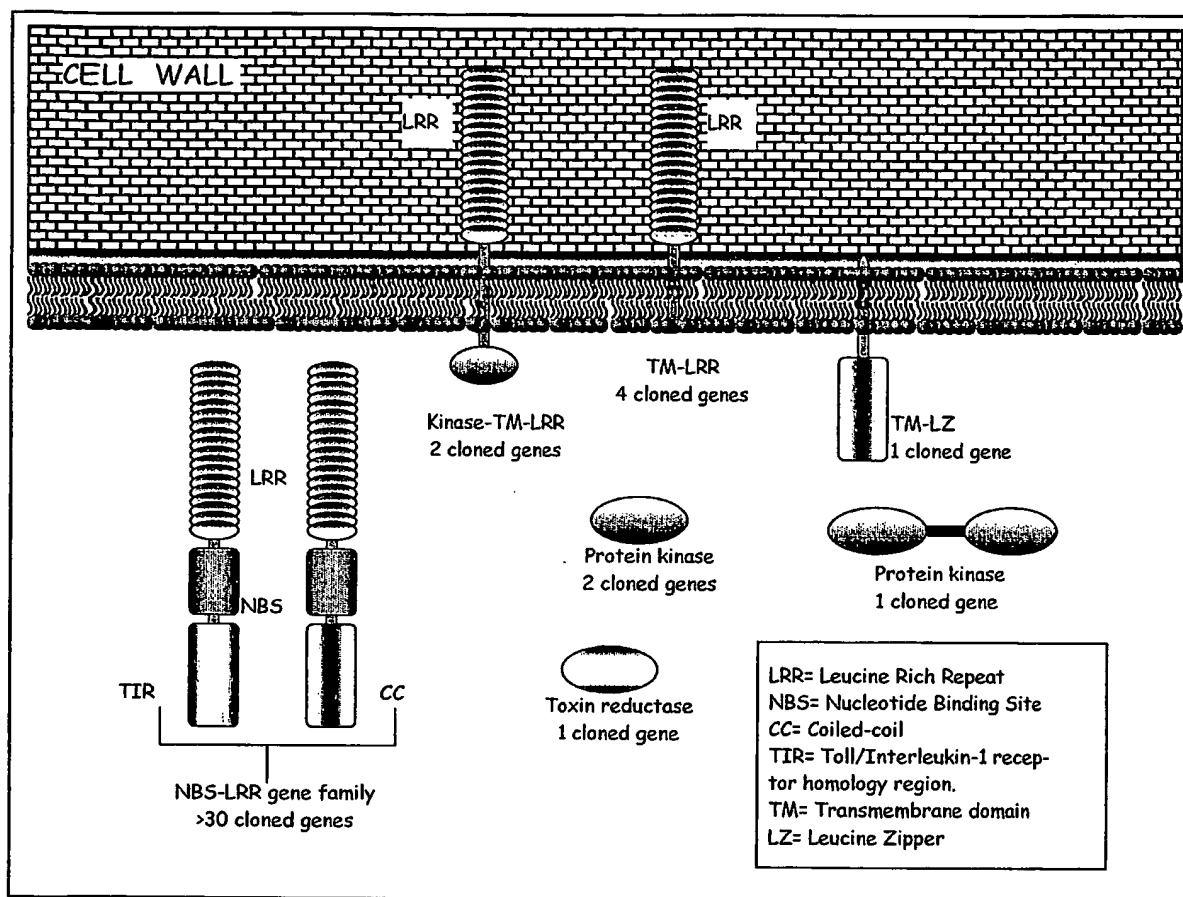


FIGURE 1

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		10	20	30	40	50	60	
RGA5	1	MSTALVIGGWFAOSFIQTLLDKASNCATQOLARRRGLHDDRRIRTSLLRIHAILDKAET	60					
RGA2	1	-MADVTPQAAAVFSLVNEIFNRSINLIVAEIRLOLNARAEINNIQRTLLRTHSLLEEAKA	59					
		70	80	90	100	110	120	
RGA5	61	RWNHKNTSLVELVROLKDAAYDAEDLLELEYQAAKQVEHRGDOISDLFSLSLSTASEW	120					
RGA2	60	RR-MTDKSLVLWLMELEKEWAYDADDILDEYFAAAIRLKVTR---S-----TKRLIDHVI	110					
		130	140	150	160	170	180	
RGA5	121	LGADGDDAGTRLREIQGKLCNIAADMMDVMQLLAPDDGGROFDWKVVRRETSSELTETVV	180					
RGA2	111	LNVP---LAHKVADIRKRLNGVTLERELNLGALE---GSOPLDS-TRKGVTTSSLTESCI	163					
		190	200	210	220	230	240	
RGA5	181	EGRDQEREKVVLELLDSGSGNSSFSVLPLVGIGGVGKTTLAQLVYNDNRVGNVYFHLKVVV	240					
RGA2	164	VGRAQDKENLIRLLLEPSDG--AVPVVPLVGLGAGKTTLSQLIFNDKRVEEHFPLRMVV	221					
		250	260	270	280	290	300	
RGA5	241	CVSDNFNVKRLTKETIESATKVEQSDKLNLDTLQQLKEKIASERFLLVLDDVWSENRDD	300					
RGA2	222	CVSDDEDVKRITREITEYATNGRFMDLTNLMLOVNLKEEIRGTTFLVLDDVWNEDPVK	281					
		310	320	330	340	350	360	
RGA5	301	WERLCAPLRFARGSKVIVTTRDTKTIASITGMTKEISLDGLQDDAYWELFKKCAFSGVN-	359					
RGA2	282	WESLLAPLDAGGRGSVVIVTTSKKVADVDTGMTPEYVLEELTEDDSWSLIESHSFREASC	341					
		370	380	390	400	410	420	
RGA5	360	POEHLELEVIGRKIAGRLKGSPLAAKTLGSLRLLDVSOEHWRTIMESEVWOLPOAENETL	419					
RGA2	342	SSTNPRMEEIGRKIAKKISGLPYGATAMGRYLRSKHGESSWREVLETETWEMPPAASDVL	401					
		430	440	450	460	470	480	
RGA5	420	PVLWLSYQHLPGHLROCFACFAVEHKDYLFIYHELIQTWIAEGFTIAHQGNKRMEDVGSSY	479					
RGA2	402	SALRRSYDNLPPOLKLCFAFCALFTKGYRFRKDTLIHMMWIAONLIQSTESKRSELMAEEC	461					
		490	500	510	520	530	540	
RGA5	480	FHEIVNRSFFQESRWRCGRYVMHDLIHDLAQELISVGECHRIIDDKSKETPSTTRILSVALT	539					
RGA2	462	FDDLVCREFEFRYS--WGNYVMNLSVHDLARWWSLDEYFRAEDUSPLHISKPIRHLSWCSE	519					
		550	560	570	580	590	600	
RGA5	540	EQMKLVDFSGYN-KLRTLMINNORNOQPYMTKVNSCLIPHSLEFKRLKRIHVLVLQKCGMK	598					
RGA2	520	RITNVLEDNNTGGDAVNPLSSLRITLLELGQSEFRSYHLDRMERMLSRIRVLDSENCVIR	579					

FIGURE 2-1

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		610	620	630	640	650	660	
RGA5	599	ELPDITGDLTQLRYLDISYNACTQRLPESLCDLYNLQALRLWGCQLRSPFQGM SKLINLR	658					
RGA2	580	NLPSSVGNLKHILRYLGLS-NTRIQLRPESVTRCLLQTLILLECCELCRIPRSMRILVKLR	638					
		670	680	690	700	710	720	
RGA5	659	QLRVEDEITISKIYEVGKLISLOELSAFKVLNNHGNKLAELSGLTQLRSTLRITNLENVGS	718					
RGA2	639	QLKANPDVIADI AKVGRLLIELQELKAYNVDKKKKGHGAELSAMNQLHGDLSIRNLQNV EK	698					
		730	740	750	760	770	780	
RGA5	719	KELASKAKILHRKQYILEALEEWAAGOVSSLEHELLVSEEVLLGLQPHHFLKSLTIRGYSG	778					
RGA2	699	TRESRKARLDEKOKIKLLDLRWADGRG---AGECDRDRKVLKGLRPHPNLRELSTIKYYGG	755					
		790	800	810	820	830	840	
RGA5	779	ATVPSWLDVKMLPNLGLTKLENCTRLEGLSYIGOLPHLKVLMKRMFVVKOMSHELCGCT	838					
RGA2	756	TSSPSWMTDOYLPNMETIRLRSCARLTELGLGOLHILRHLLHDGMSQVRCINLOFYGTG	815					
		850	860	870	880	890	900	
RGA5	839	KSKLFRLEELVLEDMPTLKEFFNLAQPLCKIIHMKNMFAVKHIGRELYGDIESNCFLS	898					
RGA2	816	EVSGFELLELINIRRMFSLEEWS-----EP	840					
		910	920	930	940	950	960	
RGA5	899	LEELVLQDMLTLEELPNLGOLPHLKVIMKNMSALKLIGRELCDSPREKIWFPRLEVLVLK	958					
RGA2	840	-----R-----RNCCTEPR-----	849					
		970	980	990	1000	1010	1020	
RGA5	959	NMLALEELPSLDNFRVSRFFASSVEVGHLFSATRKNKWFPRLEELEIKGMLTFEELHSLE	1018					
RGA2	849	-----LH-----	851					
		1030	1040	1050	1060	1070	1080	
RGA5	1019	KLPCCLKVFRIKGLPAVKKIGHGLFDSTCQRECPRLEDVLVSDMPAWEESWAEREELFS	1078					
RGA2	851	-----	851					
		1090	1100	1110	1120	1130	1140	
RGA5	1079	CLCRIKIEQCEPKLKCLLPPIPHSLIKLELWQVGLTGLPGLCKGIGGSSSTRTASLSLHII	1138					
RGA2	851	---KLLIEDCERLRNLPSLPPTLEELRISRTGLVDLPG-FH--GNQDVTNTNVSLSLHVS	905					
		1150	1160	1170	1180	1190	1200	
RGA5	1139	KCPNLRNLGEGLLSNHLPHTNAIRIWECAELLWLFPVKRFREFTTLENLSTRNCPKLM SMT	1198					
RGA2	906	ECRELRSISEGLLOHNLVALKTAFTDCDSLEELPAEGFRATSLLESIMTNCPLCS	963					

FIGURE 2-2

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		1210	1220	1230	1240	1250	1260	
							
RGA5	1199	QCEENDL	LLFPLIKALEL	GDCG--	NLGKSL	PGCLHNLSS	LQLAISN	CPYMVSLPREVM 1255
RGA2	963	-----	FLLPSSLEHL	KLPCLYPNN	NEDST	STCFENL	TSLSFTDIK	DCPNLSSFPGPPL 1017
		1270	1280	1290	1300	1310	1320	
							
RGA5	1256	LHLKEL	GTAVRTENC	DGLGST	EGLOVLK	SLKRLAT	IGCPRL	LNE-----GDEQGEVLS 1308
RGA2	1018	COLSAL	QHLSTLVN	CORLOS	IG-EQAL	TSLES	LTIQNC	PRLTMSHSLVEVNNSSDTGLAFN 1076
		1330	1340	1350	1360	1370	1380	
							
RGA5	1309	LLELSV	DKT---A	LLKLSL	IKN-----	TLPF	FIHSLR	IWSPQKVMFDLEEQLVHS 1356
RGA2	1077	ITRWM	RRRTG	DDGLML	RHRAQ	ND	SFFGGL	LQHLTFLQFLKICQCPQLVTFTGEEEKWRN 1136
		1390	1400	1410	1420	1430	1440	
							
RGA5	1357	LTATRR	TEEF	RCKNL	QSLP	TE	LHTLPS	LHATVWSDCPQIQSLPEKGLPTLLTDLGFDHCH 1416
RGA2	1137	ITS	IQILH	IVDC	PNLE	VLPAN	LQSLCS	LSLTYIVRCPRTHAFEPGGVSMSLAHVVIHECP 1196
		1450	1460	1470				
							
RGA5	1417	PVLT---	AQLEK	HLAEMK--	SSGRF	HPVYA---	1441	
RGA2	1197	QLCQ	RCDP	PGGDD	WPLIAN	VPRIC	LGRTHPCRCSTT 1232	

FIGURE 2-3

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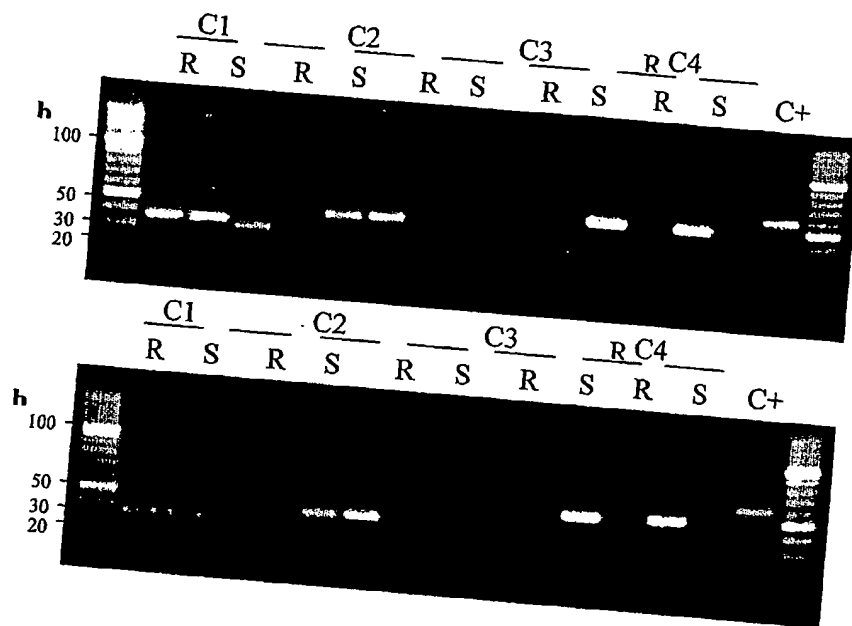


FIGURE 3